FIGURE 1

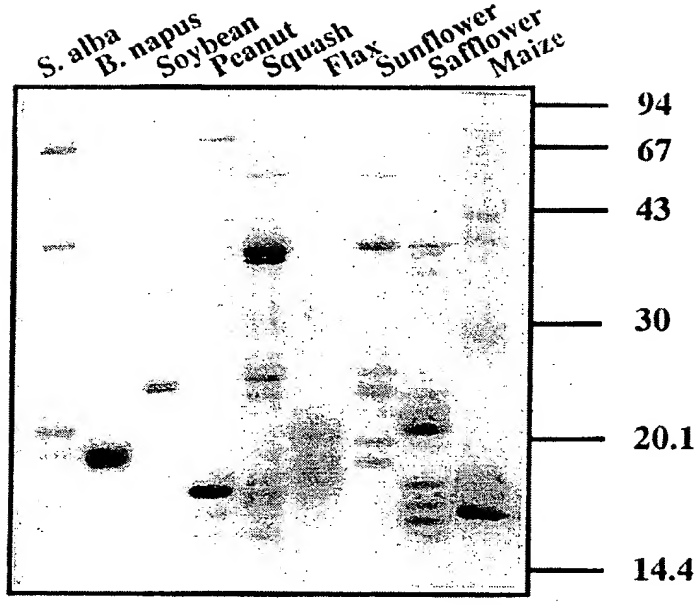
S. alba
B. napus
Soybean
Peanut
Squash
Flax
Sunflower
Safflower
Maize
94
67
43
30
20.1
14.4

FIGURE 2

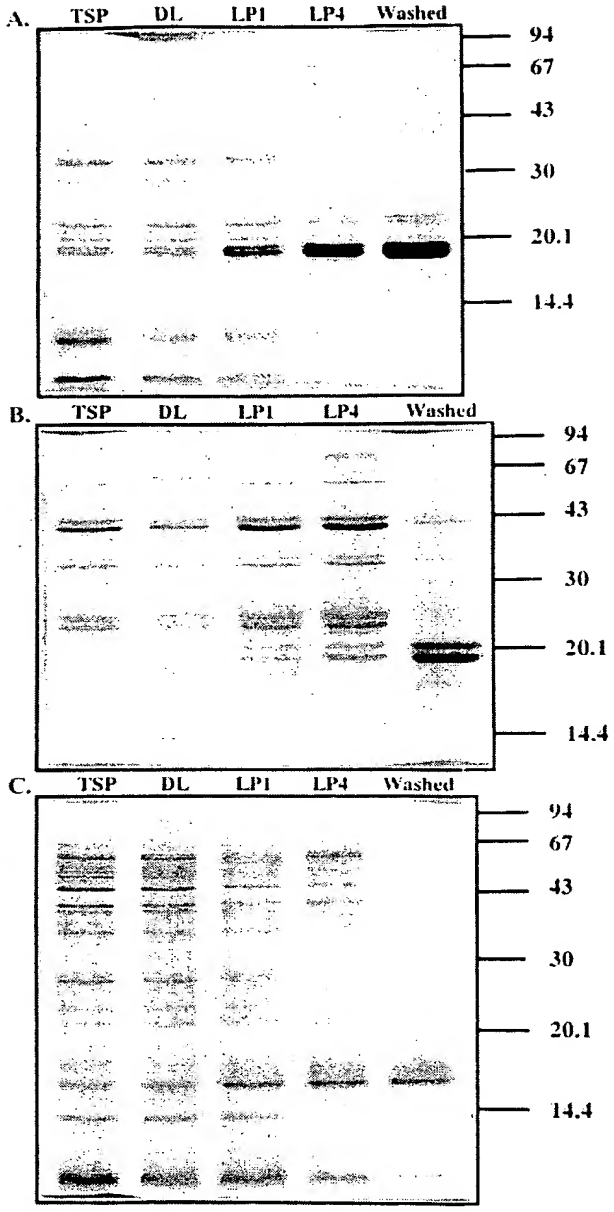
A.
TSP
DL
LP1
LP4
Washed
94
67
43
30
20.1
14.4
B.
TSP
DL
LP1
LP4
Washed
94
67
43
30
20.1
14.4
C.
TSP
DL
LP1
LP4
Washed
94
67
43
30
20.1
14.4

FIGURE 3

ClustalW Formatted Alignments

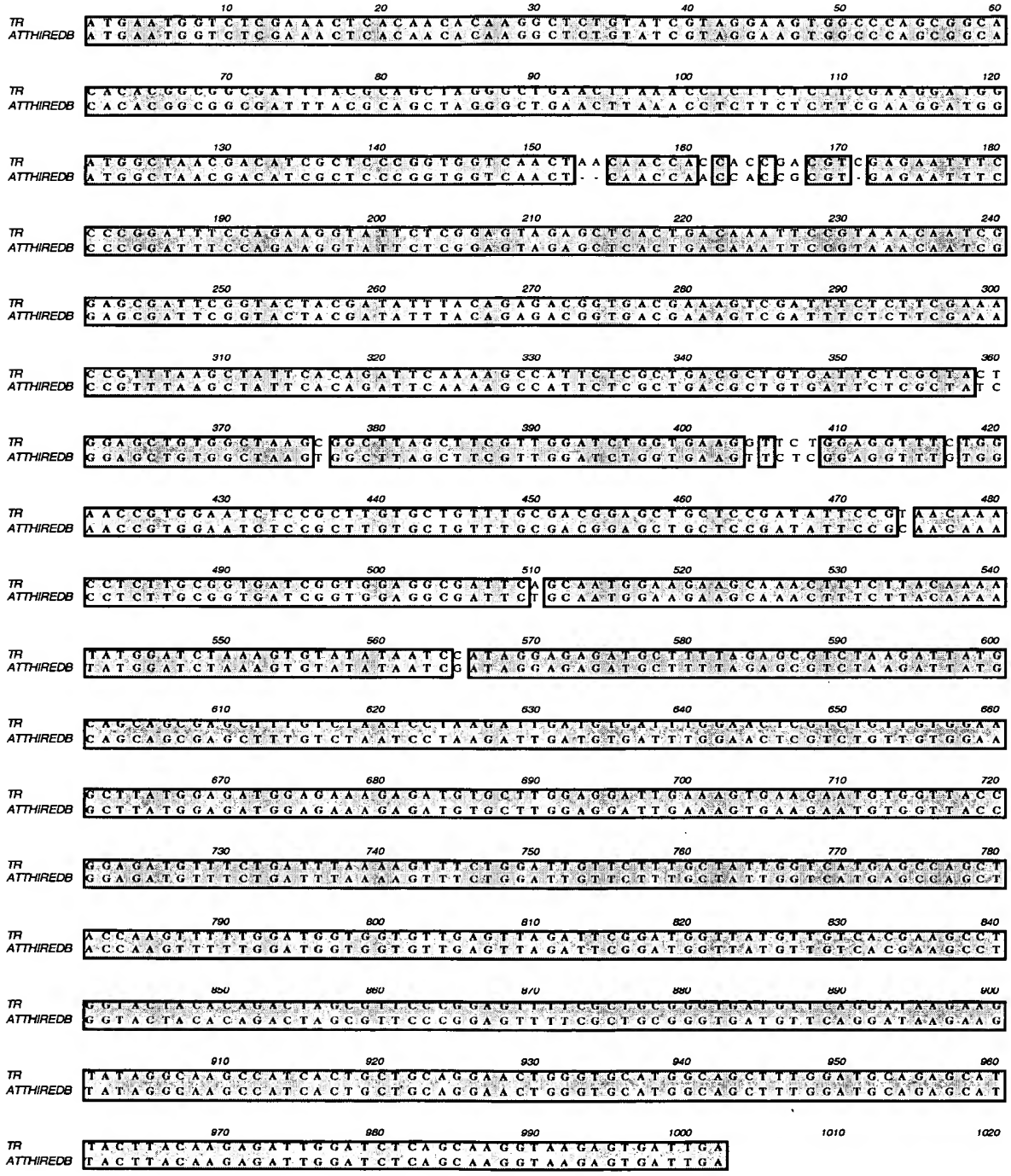

FIGURE 4

```
  1 ATG AAT GGT CTC GAA ACT CAC AAC ACA AGG CTC TGT ATC GTA GGA AGT GGC CCA GCG GCA   60
  1 M   N   G   L   E   T   H   N   T   R   L   C   I   V   G   S   G   P   A   A    20

 61 CAC ACG GCG GCG ATT TAC GCA GCT AGG GCT GAA CTT AAA CCT CTT CTC TTC GAA GGA TGG  120
 21 H   T   A   A   I   Y   A   A   R   A   E   L   K   P   L   L   F   E   G   W    40

121 ATG GCT AAC GAC ATC GCT CCC GGT GGT CAA CTA ACA ACC ACC ACC GAC GTC GAG AAT TTC  180
 41 M   A   N   D   I   A   P   G   G   Q   L   T   T   T   T   D   V   E   N   F    60

181 CCC GGA TTT CCA GAA GGT ATT CTC GGA GTA GAG CTC ACT GAC AAA TTC CGT AAA CAA TCG  240
 61 P   G   F   P   E   G   I   L   G   V   E   L   T   D   K   F   R   K   Q   S    80

241 GAG CGA TTC GGT ACT ACG ATA TTT ACA GAG ACG GTG ACG AAA GTC GAT TTC TCT TCG AAA  300
 81 E   R   F   G   T   T   I   F   T   E   T   V   T   K   V   D   F   S   S   K   100

301 CCG TTT AAG CTA TTC ACA GAT TCA AAA GCC ATT CTC GCT GAC GCT GTG ATT CTC GCT ACT  360
101 P   F   K   L   F   T   D   S   K   A   I   L   A   D   A   V   I   L   A   T   120

361 GGA GCT GTG GCT AAG CGG CTT AGC TTC GTT GGA TCT GGT GAA GGT TCT GGA GGT TTC TGG  420
121 G   A   V   A   K   R   L   S   F   V   G   S   G   E   G   S   G   G   F   W   140

421 AAC CGT GGA ATC TCC GCT TGT GCT GTT TGC GAC GGA GCT GCT CCG ATA TTC CGT AAC AAA  480
141 N   R   G   I   S   A   C   A   V   C   D   G   A   A   P   I   F   R   N   K   160

481 CCT CTT GCG GTG ATC GGT GGA GGC GAT TCA GCA ATG GAA GAA GCA AAC TTT CTT ACA AAA  540
161 P   L   A   V   I   G   G   G   D   S   A   M   E   E   A   N   F   L   T   K   180

541 TAT GGA TCT AAA GTG TAT ATA ATC CAT AGG AGA GAT GCT TTT AGA GCG TCT AAG ATT ATG  600
181 Y   G   S   K   V   Y   I   I   H   R   R   D   A   F   R   A   S   K   I   M   200

601 CAG CAG CGA GCT TTG TCT AAT CCT AAG ATT GAT GTG ATT TGG AAC TCG TCT GTT GTG GAA  660
201 Q   Q   R   A   L   S   N   P   K   I   D   V   I   W   N   S   S   V   V   E   220

661 GCT TAT GGA GAT GGA GAA AGA GAT GTG CTT GGA GGA TTG AAA GTG AAG AAT GTG GTT ACC  720
221 A   Y   G   D   G   E   R   D   V   L   G   G   L   K   V   K   N   V   V   T   240

721 GGA GAT GTT TCT GAT TTA AAA GTT TCT GGA TTG TTC TTT GCT ATT GGT CAT GAG CCA GCT  780
241 G   D   V   S   D   L   K   V   S   G   L   F   F   A   I   G   H   E   P   A   260

781 ACC AAG TTT TTG GAT GGT GGT GTT GAG TTA GAT TCG GAT GGT TAT GTT GTC ACG AAG CCT  840
261 T   K   F   L   D   G   G   V   E   L   D   S   D   G   Y   V   V   T   K   P   280

841 GGT ACT ACA CAG ACT AGC GTT CCC GGA GTT TTC GCT GCG GGT GAT GTT CAG GAT AAG AAG  900
281 G   T   T   Q   T   S   V   P   G   V   F   A   A   G   D   V   Q   D   K   K   300

901 TAT AGG CAA GCC ATC ACT GCT GCA GGA ACT GGG TGC ATG GCA GCT TTG GAT GCA GAG CAT  960
301 Y   R   Q   A   I   T   A   A   G   T   G   C   M   A   A   L   D   A   E   H   320

961 TAC TTA CAA GAG ATT GGA TCT CAG CAA GGT AAG AGT GAT TGA                         1002
321 Y   L   Q   E   I   G   S   Q   Q   G   K   S   D   *                          334
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WO 00/50576 PCT/US00/04680

FIGURE 5

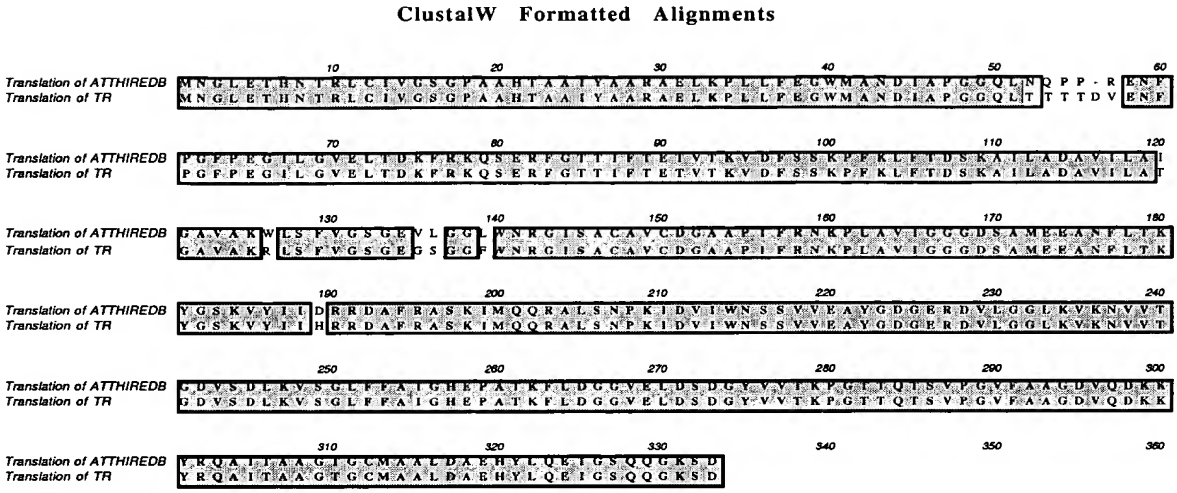
ClustalW Formatted Alignments
Translation of ATTHIREDB
Translation of TR

FIGURE 6

PstI

```
    1 ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtggtttttttacctctattta  80

   81 aaggggttttccacctaaaaattctggtatcattctcactttacttgttactttaatttctcataatctttggttgaaat 160

  161 tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaattttatgaagtc 240

  241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaattttagcgttggtagaaagcataa 320

  321 tgatttattcttattcttcttcatataaatgtttaatatacaatataaacaaattctttaccttaagaaggatttcccat 400

  401 tttatattttaaaaatatatttatcaaatatttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataa 480

  481 aatttaactccataatttttttattcgactgatcttaaagcaacacccagtgacacaactagccatttttttctttgaat 560

  561 aaaaaaatccaattatcattgtatttttttttatacaatgaaaatttcaccaaacaatcatttgtggtatttctgaagcaa 640

  641 gtcatgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

  721 cttctaaagtaatttttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

  801 ttagatataattaaaatattacttttttaattttaagtttaattgttgaatttgtgactattgatttattattctactat 880

  881 gtttaaattgttttatagatagtttaaagtaaatataagtaatgtagtagagtgttagagtgttaccctaaaccataaac 960

  961 tataagatttatggtggactaattttcatatatttcttattgcttttacctttttcttggtatgtaagtccgtaactggaa 1040

 1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

 1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

 1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcacccatctcaacccacacaca 1280

 1281 aacacattgccttttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcactt 1360

 1361 caacacacgtcaacctgcatatgcgtgtcatcccatgcccaaatctccatgcatgttccaaccaccttctctcttatata 1440

 1441 atacctataaatacctctaatatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520

 1521 ccccaacccaactcatattcaatactactctact ATG GCT TCG GAA GAA GGA CAA GTG ATC GCC TGC   1587
    1                                    M   A   S   E   E   G   Q   V   I   A   C     11

 1588 CAC ACC GTT GAG ACA TGG AAC GAG CAG CTT CAG AAG GCT AAT GAA TCC AAA ACT CTT GTG   1647
   12 H   T   V   E   T   W   N   E   Q   L   Q   K   A   N   E   S   K   T   L   V    31

 1648 GTG GTT GAT TTC ACG GCT TCT TGG TGT GGA CCA TGT CGT TTC ATC GCT CCA TTC TTT GCT   1707
   32 V   V   D   F   T   A   S   W   C   G   P   C   R   F   I   A   P   F   F   A    51

 1708 GAT TTG GCT AAG AAA CTT CCT AAC GTG CTT TTC CTC AAG GTT GAT ACT GAT GAA TTG AAG   1767
   52 D   L   A   K   K   L   P   N   V   L   F   L   K   V   D   T   D   E   L   K    71
```

FIGURE 6 (CONT'D)

```
1768 TCG GTG GCA AGT GAT TGG GCG ATA CAG GCG ATG CCA ACC TTC ATG TTT TTG AAG GAA GGG  1827
  72 S   V   A   S   D   W   A   I   Q   A   M   P   T   F   M   F   L   K   E   G    91

1828 AAG ATT TTG GAC AAA GTT GTT GGA GCC AAG AAA GAT GAG CTT CAG TCT ACC ATT GCC AAA  1887
  92 K   I   L   D   K   V   V   G   A   K   K   D   E   L   Q   S   T   I   A   K   111
                 HindIII
1888 CAC TTG GCT TAA gcttaataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgt 1963
 112 H   L   A   *                                                                   115

1964 atccgaccatgtaacagtataataactgagctccatctcacttcttctatgaataaacaaaggatgttatgatatattaa 2043

2044 cactctatctatgcaccttattgttctatgataaatttcctcttattattataaatcatctgaatcgtgacggcttatgg 2123

2124 aatgcttcaaatagtacaaaaacaaatgtgtactataagactttctaaacaattctaactttagcattgtgaacgagaca 2203

2204 taagtgttaagaagacataacaattataatggaagaagtttgtctccatttatatattatatattacccacttatgtatt 2283

2284 atattaggatgttaaggagacataacaattataaagagagaagtttgtatccatttatatattatatactacccatttat 2363

2364 atattatacttatccacttatttaatgtctttataaggtttgatccatgatatttctaatattttagttgatatgtatat 2443

2444 gaaagggtactatttgaactctcttactctgtataaaggttggatcatccttaaagtgggtctatttaattttattgctt 2523

2524 cttacagataaaaaaaaaattatgagttggtttgataaaatattgaaggatttaaaataataataaataataaataacat 2603

2604 ataatatatgtatataaatttattataatataacatttatctataaaaaagtaaatattgtcataaatctatacaatcgt 2683

2684 ttagccttgctggacgactctcaattatttaaacgagagtaaacatatttgacttttggttatttaacaaattattatt 2763

2764 taacactatatgaaatttttttttttttatcggcaaggaaataaaattaaattaggagggacaatggtgtgtcccaatcct 2843

2844 tatacaaccaacttccacaggaaggtcaggtcggggacaacaaaaaaacaggcaagggaaatttttttaatttgggttgtc 2923

2924 ttgtttgctgcataatttatgcagtaaaacactacacataaccctttttagcagtagagcaatggttgaccgtgtgcttag 3003

3004 cttcttttattttatttttttatcagcaaagaataaataaaataaaatgagacacttcagggatgtttcaacccttatac 3083

3084 aaaaccccaaaaacaagtttcctagcaccctaccaactaaggtacc                                   3129
                                                    KpnI
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09865.0008-00000

FIGURE 7

PstI

```
   1 ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtggtttttttacctctattta  80

  81 aaggggttttccacctaaaaattctggtatcattctcactttacttgttactttaatttctcataatctttggttgaaat 160

 161 tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaatttttatgaagtc 240

 241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaattttagcgttggtagaaagcataa 320

 321 tgatttattcttattcttcttcatataaatgtttaatatacaatataaacaaattctttaccttaagaaggatttcccat 400

 401 tttatattttaaaaatatatttatcaaatatttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataa 480

 481 aatttaactccataatttttttattcgactgatcttaaagcaacacccagtgacacaactagccatttttttctttgaat 560

 561 aaaaaaatccaattatcattgtatttttttttatacaatgaaaatttcaccaaacaatcatttgtggtatttctgaagcaa 640

 641 gtcatgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

 721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

 801 ttagatataattaaaatattacttttttaattttaagtttaattgttgaatttgtgactattgatttattattctactat 880

 881 gtttaaattgttttatagatagtttaaagtaaatataagtaatgtagtagagtgttagagtgttaccctaaaccataaac 960

 961 tataagatttatggtggactaattttcatatatttcttattgcttttacctttttcttggtatgtaagtccgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcacccatctcaacccacacaca 1280

1281 aacacattgccttttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgcccaaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaatacctctaatatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520

1521 ccccaacccaactcatattcaatactactctact ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT    1587
   1                                    M   A   D   T   A   R   G   T   H   H   D     11

1588 ATC ATC GGC AGA GAC CAG TAC CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC  1647
  12 I   I   G   R   D   Q   Y   P   M   M   G   R   D   R   D   Q   Y   Q   M   S    31

1648 GGA CGA GGA TCT GAC TAC TCC AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA  1707
  32 G   R   G   S   D   Y   S   K   S   R   Q   I   A   K   A   A   T   A   V   T    51

1708 GCT GGT GGT TCC CTC CTT GTT CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG  1767
  52 A   G   G   S   L   L   V   L   S   S   L   T   L   V   G   T   V   I   A   L    71
```

US 6,506,566 B1

FIGURE 7 (CONT'D)

```
1768 ACT GTT GCA ACA CCT CTG CTC GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA 1827
  72 T   V   A   T   P   L   L   V   I   F   S   P   I   L   V   P   A   L   I   T   91

1828 GTT GCA CTC CTC ATC ACC GGT TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC 1887
  92 V   A   L   L   I   T   G   F   L   S   S   G   G   F   G   I   A   A   I   T  111

1888 GTT TTC TCT TGG ATT TAC AA gtaagcacacatttatcatcttacttcataattttgtgcaatatgtgcatgca 1960
 112 V   F   S   W   I   Y   K                                                       118

1961 tgtgttgagccagtagctttggatcaatttttttggtcgaataacaaatgtaacaataagaaattgcaaattctagggaa 2040

2041 catttggttaactaaatacgaaatttgacctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaatgctt 2120

2121 ggtatgatacctattgattgtgaatag G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG     2184
 119                             Y   A   T   G   E   H   P   Q   G   S   D   K       130

2185 TTG GAC AGT GCA AGG ATG AAG TTG GGA AGC AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG 2244
 131 L   D   S   A   R   M   K   L   G   S   K   A   Q   D   L   K   D   R   A   Q   150

2245 TAC TAC GGA CAG CAA CAT ACT GGT GGG GAA CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG 2304
 151 Y   Y   G   Q   Q   H   T   G   G   E   H   D   R   D   R   T   R   G   G   Q   170
                NcoI
2305 CAC ACT ACC ATG GCT TCG GAA GAA GGA CAA GTG ATC GCC TGC CAC ACC GTT GAG ACA TGG 2364
 171 H   T   T   M   A   S   E   E   G   Q   V   I   A   C   H   T   V   E   T   W   190

2365 AAC GAG CAG CTT CAG AAG GCT AAT GAA TCC AAA ACT CTT GTG GTG GTT GAT TTC ACG GCT 2424
 191 N   E   Q   L   Q   K   A   N   E   S   K   T   L   V   V   V   D   F   T   A   210

2425 TCT TGG TGT GGA CCA TGT CGT TTC ATC GCT CCA TTC TTT GCT GAT TTG GCT AAG AAA CTT 2484
 211 S   W   C   G   P   C   R   F   I   A   P   F   F   A   D   L   A   K   K   L   230

2485 CCT AAC GTG CTT TTC CTC AAG GTT GAT ACT GAT GAA TTG AAG TCG GTG GCA AGT GAT TGG 2544
 231 P   N   V   L   F   L   K   V   D   T   D   E   L   K   S   V   A   S   D   W   250

2545 GCG ATA CAG GCG ATG CCA ACC TTC ATG TTT TTG AAG GAA GGG AAG ATT TTG GAC AAA GTT 2604
 251 A   I   Q   A   M   P   T   F   M   F   L   K   E   G   K   I   L   D   K   V   270

2605 GTT GGA GCC AAG AAA GAT GAG CTT CAG TCT ACC ATT GCC AAA CAC TTG GCT TAA gcttaata 2666
 271 V   G   A   K   K   D   E   L   Q   S   T   I   A   K   H   L   A   *           288

2667 agtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataata 2746

2747 actgagctccatctcacttcttctatgaataaacaaaggatgttatgatatattaacactctatctatgcaccttattgt 2826

2827 tctatgataaatttcctcttattattataaatcatctgaatcgtgacggcttatggaatgcttcaaatagtacaaaaaca 2906

2907 aatgtgtactataagactttctaaacaattctaactttagcattgtgaacgagacataagtgttaagaagacataacaat 2986

2987 tataatggaagaagtttgtctccatttatatattatatattacccacttatgtattatattaggatgttaaggagacata 3066
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Docket No. 5650-0360

FIGURE 7 (CONT'D)

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3067 acaattataaagagagaagtttgtatccatttatatattatatactacccatttatatattatacttatccacttattta 3146

3147 atgtctttataaggtttgatccatgatatttctaatattttagttgatatgtatatgaaagggtactatttgaactctct 3226

3227 tactctgtataaaggttggatcatccttaaagtgggtctatttaattttattgcttcttacagataaaaaaaaaattatg 3306

3307 agttggtttgataaaatattgaaggatttaaaataataataaataataaataacatataatatatgtatataaatttatt 3386

3387 ataatataacatttatctataaaaaagtaaatattgtcataaatctatacaatcgtttagccttgctggacgactctcaa 3466

3467 ttatttaaacgagagtaaacatatttgacttttggttatttaacaaattattatttaacactatatgaaatttttttt 3546

3547 tttatcggcaaggaaataaaattaaattaggagggacaatggtgtgtcccaatccttatacaaccaacttccacaggaag 3626

3627 gtcaggtcggggacaacaaaaaaacaggcaagggaaatttttaatttgggttgtcttgtttgctgcataatttatgcag 3706

3707 taaaacactacacataacccttttagcagtagagcaatggttgaccgtgtgcttagcttcttttatttatttttttatc 3786

3787 agcaaagaataaataaaataaaatgagacacttcagggatgtttcaacccttatacaaaaccccaaaaacaagtttccta 3866

3867 gcaccctaccaactaaggtacc                                                          3888
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KpnI

PCT/US2000/26020

FIGURE 8

```
    PstI
  1 ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtggtttttttacctctattta  80

 81 aaggggttttccacctaaaaattctggtatcattctcactttacttgttactttaatttctcataatctttggttgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaatttttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaattttagcgttggtagaaagcataa 320

321 tgatttattcttattcttcttcatataaatgtttaatatacaatataaacaaattctttaccttaagaaggatttcccat 400

401 tttatattttaaaaatatatttatcaaatatttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataa 480

481 aatttaactccataatttttttattcgactgatcttaaagcaacacccagtgacacaactagccatttttttctttgaat 560

561 aaaaaaatccaattatcattgtatttttttttatacaatgaaaatttcaccaaacaatcatttgtggtatttctgaagcaa 640

641 gtcatgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

801 ttagatataattaaaatattacttttttaattttaagtttaattgttgaatttgtgactattgatttattattctactat 880

881 gtttaaattgttttatagatagtttaaagtaaatataagtaatgtagtagagtgttagagtgttaccctaaaccataaac 960

961 tataagatttatggtggactaattttcatatatttcttattgcttttacctttttcttggtatgtaagtccgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcacccatctcaacccacacaca 1280

1281 aacacattgccttttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgcccaaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaatacctctaatatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520

1521 ccccaacccaactcatattcaatactactctact ATG GCT TCG GAA GAA GGA CAA GTG ATC GCC TGC   1587
   1                                    M   A   S   E   E   G   Q   V   I   A   C    11

1588 CAC ACC GTT GAG ACA TGG AAC GAG CAG CTT CAG AAG GCT AAT GAA TCC AAA ACT CTT GTG  1647
  12 H   T   V   E   T   W   N   E   Q   L   Q   K   A   N   E   S   K   T   L   V   31

1648 GTG GTT GAT TTC ACG GCT TCT TGG TGT GGA CCA TGT CGT TTC ATC GCT CCA TTC TTT GCT  1707
  32 V   V   D   F   T   A   S   W   C   G   P   C   R   F   I   A   P   F   F   A   51

1708 GAT TTG GCT AAG AAA CTT CCT AAC GTG CTT TTC CTC AAG GTT GAT ACT GAT GAA TTG AAG  1767
  52 D   L   A   K   K   L   P   N   V   L   F   L   K   V   D   T   D   E   L   K   71
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FIGURE 8 (CONT'D)

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1768 TCG GTG GCA AGT GAT TGG GCG ATA CAG GCG ATG CCA ACC TTC ATG TTT TTG AAG GAA GGG  1827
  72 S   V   A   S   D   W   A   I   Q   A   M   P   T   F   M   F   L   K   E   G    91

1828 AAG ATT TTG GAC AAA GTT GTT GGA GCC AAG AAA GAT GAG CTT CAG TCT ACC ATT GCC AAA  1887
  92 K   I   L   D   K   V   V   G   A   K   K   D   E   L   Q   S   T   I   A   K   111

1888 CAC TTG GCT ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT ATC ATC GGC AGA GAC CAG  1947
 112 H   L   A   M   A   D   T   A   R   G   T   H   H   D   I   I   G   R   D   Q   131

1948 TAC CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC GGA CGA GGA TCT GAC TAC  2007
 132 Y   P   M   M   G   R   D   R   D   Q   Y   Q   M   S   G   R   G   S   D   Y   151

2008 TCC AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA GCT GGT GGT TCC CTC CTT  2067
 152 S   K   S   R   Q   I   A   K   A   A   T   A   V   T   A   G   G   S   L   L   171

2068 GTT CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG ACT GTT GCA ACA CCT CTG  2127
 172 V   L   S   S   L   T   L   V   G   T   V   I   A   L   T   V   A   T   P   L   191

2128 CTC GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA GTT GCA CTC CTC ATC ACC  2187
 192 L   V   I   F   S   P   I   L   V   P   A   L   I   T   V   A   L   L   I   T   211

2188 GGT TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC GTT TTC TCT TGG ATT TAC  2247
 212 G   F   L   S   S   G   G   F   G   I   A   A   I   T   V   F   S   W   I   Y   231

2248 AA gtaagcacacatttatcatcttacttcataattttgtgcaatatgtgcatgcatgtgttgagccagtagctttggat 2326
 232 K                                                                              232

2327 caatttttttggtcgaataacaaatgtaacaataagaaattgcaaattctagggaacatttggttaactaaatacgaaat 2406

2407 ttgacctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaatgcttggtatgatacctattgattgtgaa 2486

2487 tag G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG TTG GAC AGT GCA AGG ATG      2544
 233       Y   A   T   G   E   H   P   Q   G   S   D   K   L   D   S   A   R   M      250

2545 AAG TTG GGA AGC AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG TAC TAC GGA CAG CAA CAT  2604
 251 K   L   G   S   K   A   Q   D   L   K   D   R   A   Q   Y   Y   G   Q   Q   H   270
                                                                    HindIII
2605 ACT GGT GGG GAA CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG CAC ACT ACT TAA gcttaata 2666
 271 T   G   G   E   H   D   R   D   R   T   R   G   G   Q   H   T   T   *          288

2667 agtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataata 2746

2747 actgagctccatctcacttcttctatgaataaacaaaggatgttatgatatattaacactctatctatgcaccttattgt 2826

2827 tctatgataaatttcctcttattattataaatcatctgaatcgtgacggcttatggaatgcttcaaatagtacaaaaaca 2906

2907 aatgtgtactataagactttctaaacaattctaactttagcattgtgaacgagacataagtgttaagaagacataacaat 2986

2987 tataatggaagaagtttgtctccatttatatattatatattacccacttatgtattatattaggatgttaaggagacata 3066
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FIGURE 8 (CONT'D)

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3067 acaattataaagagagaagtttgtatccatttatatattatatactacccatttatatattatacttatccacttattta 3146

3147 atgtctttataaggtttgatccatgatatttctaatattttagttgatatgtatatgaaagggtactatttgaactctct 3226

3227 tactctgtataaaggttggatcatccttaaagtgggtctatttaattttattgcttcttacagataaaaaaaaaattatg 3306

3307 agttggtttgataaaatattgaaggatttaaaataataataaataataaataacatataatatatgtatataaatttatt 3386

3387 ataatataacatttatctataaaaaagtaaatattgtcataaatctatacaatcgtttagccttgctggacgactctcaa 3466

3467 ttatttaaacgagagtaaacatatttgacttttggttatttaacaaattattatttaacactatatgaaatttttttt 3546

3547 tttatcggcaaggaaataaaattaaattaggagggacaatggtgtgtcccaatccttatacaaccaacttccacaggaag 3626

3627 gtcaggtcggggacaacaaaaaaacaggcaagggaaatttttaatttgggttgtcttgtttgctgcataatttatgcag 3706

3707 taaaacactacacataacccttttagcagtagagcaatggttgaccgtgtgcttagcttcttttatttatttttttatc 3786

3787 agcaaagaataaataaaataaaatgagacacttcagggatgtttcaacccttatacaaaaccccaaaaacaagtttccta 3866

3867 gcaccctaccaactaaggtacc                                                          3888
                    KpnI
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0660/9860 :0/050

FIGURE 9

PstI

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   1 ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtggtttttttacctctattta  80

  81 aaggggttttccacctaaaaattctggtatcattctcactttacttgttactttaatttctcataatctttggttgaaaat 160

 161 tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaattttatgaagtc 240

 241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaattttagcgttggtagaaagcataa 320

 321 tgatttattcttattcttcttcatataaatgtttaatatacaatataaacaaattctttaccttaagaaggatttcccat 400

 401 tttatattttaaaaatatatttatcaaatatttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataa 480

 481 aatttaactccataatttttttattcgactgatcttaaagcaacacccagtgacacaactagccatttttttctttgaat 560

 561 aaaaaaatccaattatcattgtatttttttttatacaatgaaaatttcaccaaacaatcatttgtggtatttctgaagcaa 640

 641 gtcatgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

 721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

 801 ttagatataattaaaatattacttttttaattttaagtttaattgttgaatttgtgactattgatttattattctactat 880

 881 gtttaaattgttttatagatagtttaaagtaaatataagtaatgtagtagagtgttagagtgttaccctaaaccataaac 960

 961 tataagatttatggtggactaattttcatatatttcttattgcttttacctttttcttggtatgtaagtccgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcacccatctcaacccacacaca 1280

1281 aacacattgccttttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgcccaaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaatacctctaatatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520

1521 ccccaacccaactcatattcaatactactctact ATG AAT GGT CTC GAA ACT CAC AAC ACA AGG CTC   1587
   1                                    M   N   G   L   E   T   H   N   T   R   L    11

1588 TGT ATC GTA GGA AGT GGC CCA GCG GCA CAC ACG GCG GCG ATT TAC GCA GCT AGG GCT GAA  1647
  12 C   I   V   G   S   G   P   A   A   H   T   A   A   I   Y   A   A   R   A   E   31

1648 CTT AAA CCT CTT CTC TTC GAA GGA TGG ATG GCT AAC GAC ATC GCT CCC GGT GGT CAA CTA  1707
  32 L   K   P   L   L   F   E   G   W   M   A   N   D   I   A   P   G   G   Q   L   51

1708 ACA ACC ACC ACC GAC GTC GAG AAT TTC CCC GGA TTT CCA GAA GGT ATT CTC GGA GTA GAG  1767
  52 T   T   T   T   D   V   E   N   F   P   G   F   P   E   G   I   L   G   V   E   71
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FIGURE 9 (CONT'D)

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1768 CTC ACT GAC AAA TTC CGT AAA CAA TCG GAG CGA TTC GGT ACT ACG ATA TTT ACA GAG ACG  1827
  72 L   T   D   K   F   R   K   Q   S   E   R   F   G   T   T   I   F   T   E   T    91

1828 GTG ACG AAA GTC GAT TTC TCT TCG AAA CCG TTT AAG CTA TTC ACA GAT TCA AAA GCC ATT  1887
  92 V   T   K   V   D   F   S   S   K   P   F   K   L   F   T   D   S   K   A   I   111

1888 CTC GCT GAC GCT GTG ATT CTC GCT ACT GGA GCT GTG GCT AAG CGG CTT AGC TTC GTT GGA  1947
 112 L   A   D   A   V   I   L   A   T   G   A   V   A   K   R   L   S   F   V   G   131

1948 TCT GGT GAA GGT TCT GGA GGT TTC TGG AAC CGT GGA ATC TCC GCT TGT GCT GTT TGC GAC  2007
 132 S   G   E   G   S   G   G   F   W   N   R   G   I   S   A   C   A   V   C   D   151

2008 GGA GCT GCT CCG ATA TTC CGT AAC AAA CCT CTT GCG GTG ATC GGT GGA GGC GAT TCA GCA  2067
 152 G   A   A   P   I   F   R   N   K   P   L   A   V   I   G   G   G   D   S   A   171

2068 ATG GAA GAA GCA AAC TTT CTT ACA AAA TAT GGA TCT AAA GTG TAT ATA ATC CAT AGG AGA  2127
 172 M   E   E   A   N   F   L   T   K   Y   G   S   K   V   Y   I   I   H   R   R   191

2128 GAT GCT TTT AGA GCG TCT AAG ATT ATG CAG CAG CGA GCT TTG TCT AAT CCT AAG ATT GAT  2187
 192 D   A   F   R   A   S   K   I   M   Q   Q   R   A   L   S   N   P   K   I   D   211

2188 GTG ATT TGG AAC TCG TCT GTT GTG GAA GCT TAT GGA GAT GGA GAA AGA GAT GTG CTT GGA  2247
 212 V   I   W   N   S   S   V   V   E   A   Y   G   D   G   E   R   D   V   L   G   231

2248 GGA TTG AAA GTG AAG AAT GTG GTT ACC GGA GAT GTT TCT GAT TTA AAA GTT TCT GGA TTG  2307
 232 G   L   K   V   K   N   V   V   T   G   D   V   S   D   L   K   V   S   G   L   251

2308 TTC TTT GCT ATT GGT CAT GAG CCA GCT ACC AAG TTT TTG GAT GGT GGT GTT GAG TTA GAT  2367
 252 F   F   A   I   G   H   E   P   A   T   K   F   L   D   G   G   V   E   L   D   271

2368 TCG GAT GGT TAT GTT GTC ACG AAG CCT GGT ACT ACA CAG ACT AGC GTT CCC GGA GTT TTC  2427
 272 S   D   G   Y   V   V   T   K   P   G   T   T   Q   T   S   V   P   G   V   F   291

2428 GCT GCG GGT GAT GTT CAG GAT AAG AAG TAT AGG CAA GCC ATC ACT GCT GCA GGA ACT GGG  2487
 292 A   A   G   D   V   Q   D   K   K   Y   R   Q   A   I   T   A   A   G   T   G   311

2488 TGC ATG GCA GCT TTG GAT GCA GAG CAT TAC TTA CAA GAG ATT GGA TCT CAG CAA GGT AAG  2547
 312 C   M   A   A   L   D   A   E   H   Y   L   Q   E   I   G   S   Q   Q   G   K   331

2548 AGT GAT TGA agcttaataagtatgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatc  2624
 332 S   D   *  HindIII                                                              334

2625 cgaccatgtaacagtataataactgagctccatctcacttcttctatgaataaacaaaggatgttatgatatattaacac  2704

2705 tctatctatgcaccttattgttctatgataaatttcctcttattattataaatcatctgaatcgtgacggcttatggaat  2784

2785 gcttcaaatagtacaaaaacaaatgtgtactataagactttctaaacaattctaactttagcattgtgaacgagacataa  2864

2865 gtgttaagaagacataacaattataatggaagaagtttgtctccatttatatattatatattacccacttatgtattata  2944
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FIGURE 9 (CONT'D)

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2945 ttaggatgttaaggagacataacaattataaagagagaagtttgtatccatttatatattatatactacccatttatata 3024

3025 ttatacttatccacttatttaatgtctttataaggtttgatccatgatatttctaatattttagttgatatgtatatgaa 3104

3105 agggtactatttgaactctcttactctgtataaaggttggatcatccttaaagtgggtctatttaattttattgcttctt 3184

3185 acagataaaaaaaaaaattatgagttggtttgataaaatattgaaggatttaaaataataataaataataaataacatata 3264

3265 atatatgtatataaatttattataatataacatttatctataaaaaagtaaatattgtcataaatctatacaatcgttta 3344

3345 gccttgctggacgactctcaattatttaaacgagagtaaacatatttgacttttggttatttaacaaattattatttaa 3424

3425 cactatatgaaatttttttttttatcggcaaggaaataaaattaaattaggagggacaatggtgtgtcccaatccttat 3504

3505 acaaccaacttccacaggaaggtcaggtcggggacaacaaaaaaacaggcaagggaaatttttaatttgggttgtcttg 3584

3585 tttgctgcataatttatgcagtaaaacactacacataacccttttagcagtagagcaatggttgaccgtgtgcttagctt 3664

3665 cttttatttttatttttttatcagcaaagaataaataaaataaaatgagacacttcagggatgtttcaacccttatacaaa 3744

3745 accccaaaaacaagtttcctagcaccctaccaactaaggtacc                                    3787
                                                KpnI
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FIGURE 10

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     PstI
   1 ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtggtttttttacctctattta  80

  81 aaggggttttccacctaaaaattctggtatcattctcactttacttgttactttaatttctcataatctttggttgaaat 160

 161 tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaatttttatgaagtc 240

 241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaatttttagcgttggtagaaagcataa 320

 321 tgatttattcttattcttcttcatataaatgtttaatatacaatataaacaaattctttaccttaagaaggatttcccat 400

 401 tttatattttaaaaatatatttatcaaatatttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataa 480

 481 aatttaactccataatttttttattcgactgatcttaaagcaacacccagtgacacaactagccatttttttctttgaat 560

 561 aaaaaaatccaattatcattgtatttttttttatacaatgaaaatttcaccaaacaatcatttgtggtatttctgaagcaa 640

 641 gtcatgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

 721 cttctaaagtaattttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

 801 ttagatataattaaaatattacttttttaattttaagtttaattgttgaatttgtgactattgatttattattctactat 880

 881 gtttaaattgttttatagatagtttaaagtaaatataagtaatgtagtagagtgttagagtgttaccctaaaccataaac 960

 961 tataagatttatggtggactaattttcatatatttcttattgcttttacctttttcttggtatgtaagtccgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcacccatctcaacccacacaca 1280

1281 aacacattgccttttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgcccaaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaataacctctaatatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520

1521 ccccaacccaactcatattcaatactactctact ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT   1587
   1                                    M   A   D   T   A   R   G   T   H   H   D     11

1588 ATC ATC GGC AGA GAC CAG TAC CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC  1647
  12 I   I   G   R   D   Q   Y   P   M   M   G   R   D   R   D   Q   Y   Q   M   S    31

1648 GGA CGA GGA TCT GAC TAC TCC AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA  1707
  32 G   R   G   S   D   Y   S   K   S   R   Q   I   A   K   A   A   T   A   V   T    51

1708 GCT GGT GGT TCC CTC CTT GTT CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG  1767
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FIGURE 10 (CONT'D)

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  52 A   G   G   S   L   L   V   L   S   S   L   T   L   V   G   T   V   I   A   L    71

1768 ACT GTT GCA ACA CCT CTG CTC GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA  1827
  72 T   V   A   T   P   L   L   V   I   F   S   P   I   L   V   P   A   L   I   T    91

1828 GTT GCA CTC CTC ATC ACC GGT TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC  1887
  92 V   A   L   L   I   T   G   F   L   S   S   G   G   F   G   I   A   A   I   T   111

1888 GTT TTC TCT TGG ATT TAC AA gtaagcacacatttatcatcttacttcataattttgtgcaatatgtgcatgca 1960
 112 V   F   S   W   I   Y   K                                                       118

1961 tgtgttgagccagtagctttggatcaatttttttggtcgaataacaaatgtaacaataagaaattgcaaattctagggaa 2040

2041 catttggttaactaaatacgaaatttgacctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaatgctt 2120

2121 ggtatgatacctattgattgtgaatag G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG     2184
 119                             Y   A   T   G   E   H   P   Q   G   S   D   K       130

2185 TTG GAC AGT GCA AGG ATG AAG TTG GGA AGC AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG  2244
 131 L   D   S   A   R   M   K   L   G   S   K   A   Q   D   L   K   D   R   A   Q   150

2245 TAC TAC GGA CAG CAA CAT ACT GGT GGG GAA CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG  2304
 151 Y   Y   G   Q   Q   H   T   G   G   E   H   D   R   D   R   T   R   G   G   Q   170

2305 CAC ACT ACC ATG AAT GGT CTC GAA ACT CAC AAC ACA AGG CTC TGT ATC GTA GGA AGT GGC  2364
 171 H   T   T   M   N   G   L   E   T   H   N   T   R   L   C   I   V   G   S   G   190

2365 CCA GCG GCA CAC ACG GCG GCG ATT TAC GCA GCT AGG GCT GAA CTT AAA CCT CTT CTC TTC  2424
 191 P   A   A   H   T   A   A   I   Y   A   A   R   A   E   L   K   P   L   L   F   210

2425 GAA GGA TGG ATG GCT AAC GAC ATC GCT CCC GGT GGT CAA CTA ACA ACC ACC ACC GAC GTC  2484
 211 E   G   W   M   A   N   D   I   A   P   G   G   Q   L   T   T   T   T   D   V   230

2485 GAG AAT TTC CCC GGA TTT CCA GAA GGT ATT CTC GGA GTA GAG CTC ACT GAC AAA TTC CGT  2544
 231 E   N   F   P   G   F   P   E   G   I   L   G   V   E   L   T   D   K   F   R   250

2545 AAA CAA TCG GAG CGA TTC GGT ACT ACG ATA TTT ACA GAG ACG GTG ACG AAA GTC GAT TTC  2604
 251 K   Q   S   E   R   F   G   T   T   I   F   T   E   T   V   T   K   V   D   F   270

2605 TCT TCG AAA CCG TTT AAG CTA TTC ACA GAT TCA AAA GCC ATT CTC GCT GAC GCT GTG ATT  2664
 271 S   S   K   P   F   K   L   F   T   D   S   K   A   I   L   A   D   A   V   I   290

2665 CTC GCT ACT GGA GCT GTG GCT AAG CGG CTT AGC TTC GTT GGA TCT GGT GAA GGT TCT GGA  2724
 291 L   A   T   G   A   V   A   K   R   L   S   F   V   G   S   G   E   G   S   G   310

2725 GGT TTC TGG AAC CGT GGA ATC TCC GCT TGT GCT GTT TGC GAC GGA GCT GCT CCG ATA TTC  2784
 311 G   F   W   N   R   G   I   S   A   C   A   V   C   D   G   A   A   P   I   F   330

2785 CGT AAC AAA CCT CTT GCG GTG ATC GGT GGA GGC GAT TCA GCA ATG GAA GAA GCA AAC TTT  2844
 331 R   N   K   P   L   A   V   I   G   G   G   D   S   A   M   E   E   A   N   F   350
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FIGURE 10 (CONT'D)

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2845 CTT ACA AAA TAT GGA TCT AAA GTG TAT ATA ATC CAT AGG AGA GAT GCT TTT AGA GCG TCT  2904
 351 L   T   K   Y   G   S   K   V   Y   I   I   H   R   R   D   A   F   R   A   S    370

2905 AAG ATT ATG CAG CAG CGA GCT TTG TCT AAT CCT AAG ATT GAT GTG ATT TGG AAC TCG TCT  2964
 371 K   I   M   Q   Q   R   A   L   S   N   P   K   I   D   V   I   W   N   S   S    390

2965 GTT GTG GAA GCT TAT GGA GAT GGA GAA AGA GAT GTG CTT GGA GGA TTG AAA GTG AAG AAT  3024
 391 V   V   E   A   Y   G   D   G   E   R   D   V   L   G   G   L   K   V   K   N    410

3025 GTG GTT ACC GGA GAT GTT TCT GAT TTA AAA GTT TCT GGA TTG TTC TTT GCT ATT GGT CAT  3084
 411 V   V   T   G   D   V   S   D   L   K   V   S   G   L   F   F   A   I   G   H    430

3085 GAG CCA GCT ACC AAG TTT TTG GAT GGT GGT GTT GAG TTA GAT TCG GAT GGT TAT GTT GTC  3144
 431 E   P   A   T   K   F   L   D   G   G   V   E   L   D   S   D   G   Y   V   V    450

3145 ACG AAG CCT GGT ACT ACA CAG ACT AGC GTT CCC GGA GTT TTC GCT GCG GGT GAT GTT CAG  3204
 451 T   K   P   G   T   T   Q   T   S   V   P   G   V   F   A   A   G   D   V   Q    470

3205 GAT AAG AAG TAT AGG CAA GCC ATC ACT GCT GCA GGA ACT GGG TGC ATG GCA GCT TTG GAT  3264
 471 D   K   K   Y   R   Q   A   I   T   A   A   G   T   G   C   M   A   A   L   D    490

3265 GCA GAG CAT TAC TTA CAA GAG ATT GGA TCT CAG CAA GGT AAG AGT GAT TGA agcttaataagt  3327
 491 A   E   H   Y   L   Q   E   I   G   S   Q   Q   G   K   S   D   *  HindIII      507

3328 atgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataataact 3407

3408 gagctccatctcacttcttctatgaataaacaaaggatgttatgatatattaacactctatctatgcaccttattgttct 3487

3488 atgataaatttcctcttattattataaatcatctgaatcgtgacggcttatggaatgcttcaaatagtacaaaaacaaat 3567

3568 gtgtactataagactttctaaacaattctaactttagcattgtgaacgagacataagtgttaagaagacataacaattat 3647

3648 aatggaagaagtttgtctccatttatatattatatattacccacttatgtattatattaggatgttaaggagacataaca 3727

3728 attataaagagagaagtttgtatccatttatatattatatactacccatttatatattatacttatccacttatttaatg 3807

3808 tctttataaggtttgatccatgatatttctaatattttagttgatatgtatatgaaagggtactatttgaactctcttac 3887

3888 tctgtataaaggttggatcatccttaaagtgggtctatttaattttattgcttcttacagataaaaaaaaaattatgagt 3967

3968 tggtttgataaaatattgaaggatttaaaataataataaataataaataacatataatatatgtatataaatttattata 4047

4048 atataacatttatctataaaaaagtaaatattgtcataaatctatacaatcgtttagccttgctggacgactctcaatta 4127

4128 tttaaacgagagtaaacatatttgacttttttggttatttaacaaattattatttaacactatatgaaatttttttttttt 4207

4208 atcggcaaggaaataaaattaaattaggagggacaatggtgtgtcccaatccttatacaaccaacttccacaggaaggtc 4287
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FIGURE 10 (CONT'D)

```
4288 aggtcggggacaacaaaaaaacaggcaagggaaatttttaatttgggttgtcttgtttgctgcataatttatgcagtaa 4367

4368 aacactacacataaccctttagcagtagagcaatggttgaccgtgtgcttagcttcttttatttttatttttttatcagc 4447

4448 aaagaataaataaaataaaatgagacacttcagggatgtttcaacccttatacaaaaccccaaaaacaagtttcctagca 4527

4528 ccctaccaactaaggtacc                                                              4546
                  KpnI
```

TOTAL P.05

FIGURE 11

```
    PstI
  1 ctgcaggaattcattgtactcccagtatcattatagtgaaagttttggctctctcgccggtggtttttttacctctattta  80

 81 aaggggttttccacctaaaaattctggtatcattctcactttacttgttactttaatttctcataatctttggttgaaat 160

161 tatcacgcttccgcacacgatatccctacaaatttattatttgttaaacattttcaaaccgcataaaatttttatgaagtc 240

241 ccgtctatctttaatgtagtctaacattttcatattgaaatatataatttacttaattttagcgttggtagaaagcataa 320

321 tgatttattcttattcttcttcatataaatgtttaatatacaatataaacaaattctttaccttaagaaggatttcccat 400

401 tttatattttaaaaatatatttatcaaatatttttcaaccacgtaaatctcataataataagttgtttcaaaagtaataa 480

481 aatttaactccataatttttttattcgactgatcttaaagcaacacccagtgacacaactagccatttttttctttgaat 560

561 aaaaaaatccaattatcattgtatttttttttatacaatgaaaatttcaccaaacaatcatttgtggtatttctgaagcaa 640

641 gtcatgttatgcaaaattctataattcccatttgacactacggaagtaactgaagatctgcttttacatgcgagacacat 720

721 cttctaaagtaatttttaataatagttactatattcaagatttcatatatcaaatactcaatattacttctaaaaaattaa 800

801 ttagatataattaaaatattacttttttaattttaagtttaattgttgaatttgtgactattgatttattattctactat 880

881 gtttaaattgttttatagatagtttaaagtaaatataagtaatgtagtagagtgttagagtgttaccctaaaccataaac 960

961 tataagatttatggtggactaattttcatatatttcttattgcttttacctttttcttggtatgtaagtccgtaactggaa 1040

1041 ttactgtgggttgccatggcactctgtggtcttttggttcatgcatggatgcttgcgcaagaaaaagacaaagaacaaag 1120

1121 aaaaaagacaaaacagagagacaaaacgcaatcacacaaccaactcaaattagtcactggctgatcaagatcgccgcgtc 1200

1201 catgtatgtctaaatgccatgcaaagcaacacgtgcttaacatgcactttaaatggctcacccatctcaacccacacaca 1280

1281 aacacattgccttttttcttcatcatcaccacaaccacctgtatatattcattctcttccgccacctcaatttcttcactt 1360

1361 caacacacgtcaacctgcatatgcgtgtcatcccatgcccaaatctccatgcatgttccaaccaccttctctcttatata 1440

1441 atacctataaatacctctaatatcactcacttctttcatcatccatccatccagagtactactactctactactataata 1520

1521 ccccaacccaactcatattcaatactactctact ATG AAT GGT CTC GAA ACT CAC AAC ACA AGG CTC   1587
   1                                    M   N   G   L   E   T   H   N   T   R   L    11

1588 TGT ATC GTA GGA AGT GGC CCA GCG GCA CAC ACG GCG GCG ATT TAC GCA GCT AGG GCT GAA  1647
  12 C   I   V   G   S   G   P   A   A   H   T   A   A   I   Y   A   A   R   A   E   31

1648 CTT AAA CCT CTT CTC TTC GAA GGA TGG ATG GCT AAC GAC ATC GCT CCC GGT GGT CAA CTA  1707
  32 L   K   P   L   L   F   E   G   W   M   A   N   D   I   A   P   G   G   Q   L   51

1708 ACA ACC ACC ACC GAC GTC GAG AAT TTC CCC GGA TTT CCA GAA GGT ATT CTC GGA GTA GAG  1767
  52 T   T   T   T   D   V   E   N   F   P   G   F   P   E   G   I   L   G   V   E   71
```

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FIGURE 11 (CONT'D)

```
1768 CTC ACT GAC AAA TTC CGT AAA CAA TCG GAG CGA TTC GGT ACT ACG ATA TTT ACA GAG ACG 1827
  72 L   T   D   K   F   R   K   Q   S   E   R   F   G   T   T   I   F   T   E   T  91

1828 GTG ACG AAA GTC GAT TTC TCT TCG AAA CCG TTT AAG CTA TTC ACA GAT TCA AAA GCC ATT 1887
  92 V   T   K   V   D   F   S   S   K   P   F   K   L   F   T   D   S   K   A   I  111

1888 CTC GCT GAC GCT GTG ATT CTC GCT ACT GGA GCT GTG GCT AAG CGG CTT AGC TTC GTT GGA 1947
 112 L   A   D   A   V   I   L   A   T   G   A   V   A   K   R   L   S   F   V   G  131

1948 TCT GGT GAA GGT TCT GGA GGT TTC TGG AAC CGT GGA ATC TCC GCT TGT GCT GTT TGC GAC 2007
 132 S   G   E   G   S   G   G   F   W   N   R   G   I   S   A   C   A   V   C   D  151

2008 GGA GCT GCT CCG ATA TTC CGT AAC AAA CCT CTT GCG GTG ATC GGT GGA GGC GAT TCA GCA 2067
 152 G   A   A   P   I   F   R   N   K   P   L   A   V   I   G   G   G   D   S   A  171

2068 ATG GAA GAA GCA AAC TTT CTT ACA AAA TAT GGA TCT AAA GTG TAT ATA ATC CAT AGG AGA 2127
 172 M   E   E   A   N   F   L   T   K   Y   G   S   K   V   Y   I   I   H   R   R  191

2128 GAT GCT TTT AGA GCG TCT AAG ATT ATG CAG CAG CGA GCT TTG TCT AAT CCT AAG ATT GAT 2187
 192 D   A   F   R   A   S   K   I   M   Q   Q   R   A   L   S   N   P   K   I   D  211

2188 GTG ATT TGG AAC TCG TCT GTT GTG GAA GCT TAT GGA GAT GGA GAA AGA GAT GTG CTT GGA 2247
 212 V   I   W   N   S   S   V   V   E   A   Y   G   D   G   E   R   D   V   L   G  231

2248 GGA TTG AAA GTG AAG AAT GTG GTT ACC GGA GAT GTT TCT GAT TTA AAA GTT TCT GGA TTG 2307
 232 G   L   K   V   K   N   V   V   T   G   D   V   S   D   L   K   V   S   G   L  251

2308 TTC TTT GCT ATT GGT CAT GAG CCA GCT ACC AAG TTT TTG GAT GGT GGT GTT GAG TTA GAT 2367
 252 F   F   A   I   G   H   E   P   A   T   K   F   L   D   G   G   V   E   L   D  271

2368 TCG GAT GGT TAT GTT GTC ACG AAG CCT GGT ACT ACA CAG ACT AGC GTT CCC GGA GTT TTC 2427
 272 S   D   G   Y   V   V   T   K   P   G   T   T   Q   T   S   V   P   G   V   F  291

2428 GCT GCG GGT GAT GTT CAG GAT AAG AAG TAT AGG CAA GCC ATC ACT GCT GCA GGA ACT GGG 2487
 292 A   A   G   D   V   Q   D   K   K   Y   R   Q   A   I   T   A   A   G   T   G  311

2488 TGC ATG GCA GCT TTG GAT GCA GAG CAT TAC TTA CAA GAG ATT GGA TCT CAG CAA GGT AAG 2547
 312 C   M   A   A   L   D   A   E   H   Y   L   Q   E   I   G   S   Q   Q   G   K  331

2548 AGT GAT ATG GCG GAT ACA GCT AGA GGA ACC CAT CAC GAT ATC ATC GGC AGA GAC CAG TAC 2607
 332 S   D   M   A   D   T   A   R   G   T   H   H   D   I   I   G   R   D   Q   Y  351

2608 CCG ATG ATG GGC CGA GAC CGA GAC CAG TAC CAG ATG TCC GGA CGA GGA TCT GAC TAC TCC 2667
 352 P   M   M   G   R   D   R   D   Q   Y   Q   M   S   G   R   G   S   D   Y   S  371

2668 AAG TCT AGG CAG ATT GCT AAA GCT GCA ACT GCT GTC ACA GCT GGT GGT TCC CTC CTT GTT 2727
 372 K   S   R   Q   I   A   K   A   A   T   A   V   T   A   G   G   S   L   L   V  391
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FIGURE 11 (CONT'D)

```
2728 CTC TCC AGC CTT ACC CTT GTT GGA ACT GTC ATA GCT TTG ACT GTT GCA ACA CCT CTG CTC  2787
 392 L   S   S   L   T   L   V   G   T   V   I   A   L   T   V   A   T   P   L   L    411

2788 GTT ATC TTC AGC CCA ATC CTT GTC CCG GCT CTC ATC ACA GTT GCA CTC CTC ATC ACC GGT  2847
 412 V   I   F   S   P   I   L   V   P   A   L   I   T   V   A   L   L   I   T   G    431

2848 TTT CTT TCC TCT GGA GGG TTT GGC ATT GCC GCT ATA ACC GTT TTC TCT TGG ATT TAC AA g 2907
 432 F   L   S   S   G   G   F   G   I   A   A   I   T   V   F   S   W   I   Y   K    451

2908 taagcacacatttatcatcttacttcataattttgtgcaatatgtgcatgcatgtgttgagccagtagctttggatcaat 2987

2988 ttttttggtcgaataacaaatgtaacaataagaaattgcaaattctagggaacatttggttaactaaatacgaaatttga 3067

3068 cctagctagcttgaatgtgtctgtgtatatcatctatataggtaaaatgcttggtatgatacctattgattgtgaatag  3146

3147 G TAC GCA ACG GGA GAG CAC CCA CAG GGA TCA GAC AAG TTG GAC AGT GCA AGG ATG AAG     3204
 452   Y   A   T   G   E   H   P   Q   G   S   D   K   L   D   S   A   R   M   K      470

3205 TTG GGA AGC AAA GCT CAG GAT CTG AAA GAC AGA GCT CAG TAC TAC GGA CAG CAA CAT ACT  3264
 471 L   G   S   K   A   Q   D   L   K   D   R   A   Q   Y   Y   G   Q   Q   H   T    490

3265 GGT GGG GAA CAT GAC CGT GAC CGT ACT CGT GGT GGC CAG CAC ACT ACT TAA gctttaataagta 3327
 491 G   G   E   H   D   R   D   R   T   R   G   G   Q   H   T   T   *   HindIII      507

3328 tgaactaaaatgcatgtaggtgtaagagctcatggagagcatggaatattgtatccgaccatgtaacagtataataactg 3407

3408 agctccatctcacttcttctatgaataaacaaaggatgttatgatatattaacactctatctatgcaccttattgttcta 3487

3488 tgataaatttcctcttattattataaatcatctgaatcgtgacggcttatggaatgcttcaaatagtacaaaaacaaatg 3567

3568 tgtactataagactttctaaacaattctaactttagcattgtgaacgagacataagtgttaagaagacataacaattata 3647

3648 atggaagaagtttgtctccatttatatattatatattacccacttatgtattatattaggatgttaaggagacataacaa 3727

3728 ttataaagagagaagtttgtatccatttatatattatatactacccatttatatattatacttatccacttatttaatgt 3807

3808 ctttataaggtttgatccatgatatttctaatattttagttgatatgtatatgaaagggtactatttgaactctcttact 3887

3888 ctgtataaaggttggatcatccttaaagtgggtctatttaattttattgcttcttacagataaaaaaaaaaattatgagtt 3967

3968 ggtttgataaaatattgaaggatttaaaataataataaataataaataacatataatatatgtatataaatttattataa 4047

4048 tataacatttatctataaaaaagtaaatattgtcataaatctatacaatcgtttagccttgctggacgactctcaattat 4127

4128 ttaaacgagagtaaacatatttgacttttggttatttaacaaattattatttaacactatatgaaatttttttttttta 4207

4208 tcggcaaggaaataaaattaaattaggagggacaatggtgtgtcccaatccttatacaaccaacttccacaggaaggtca 4287
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FIGURE 11 (CONT'D)

```
4288 ggtcggggacaacaaaaaaacaggcaagggaaatttttaatttgggttgtcttgtttgctgcataatttatgcagtaaa 4367

4368 acactacacataaccctttagcagtagagcaatggttgaccgtgtgcttagcttcttttatttttatttttttatcagca 4447

4448 aagaataaataaaataaaatgagacacttcagggatgtttcaacccttatacaaaaccccaaaaacaagtttcctagcac 4527

4528 cctaccaactaaggtacc                                                              4545
                 KpnI
```

1 0 5 0 9 0 2 6 0 9 0 5 0 1

FIGURE 12

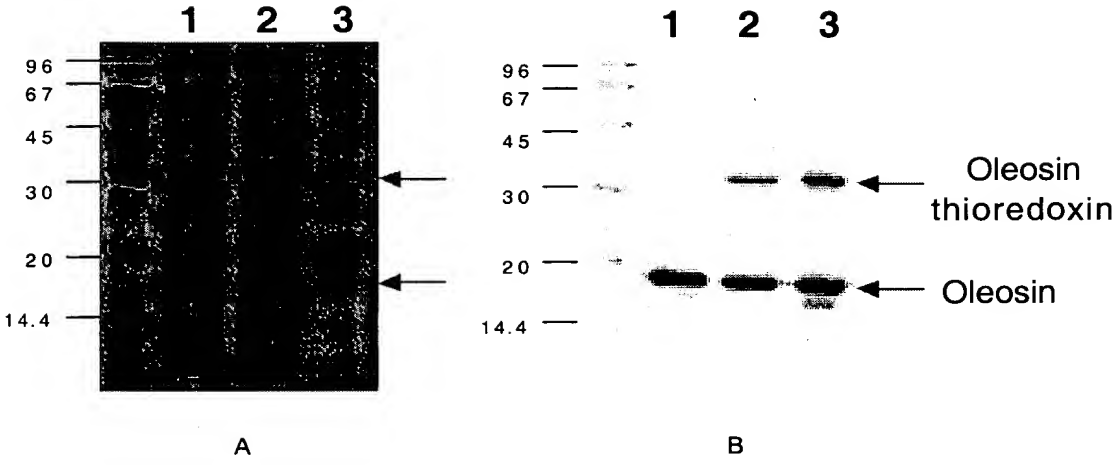
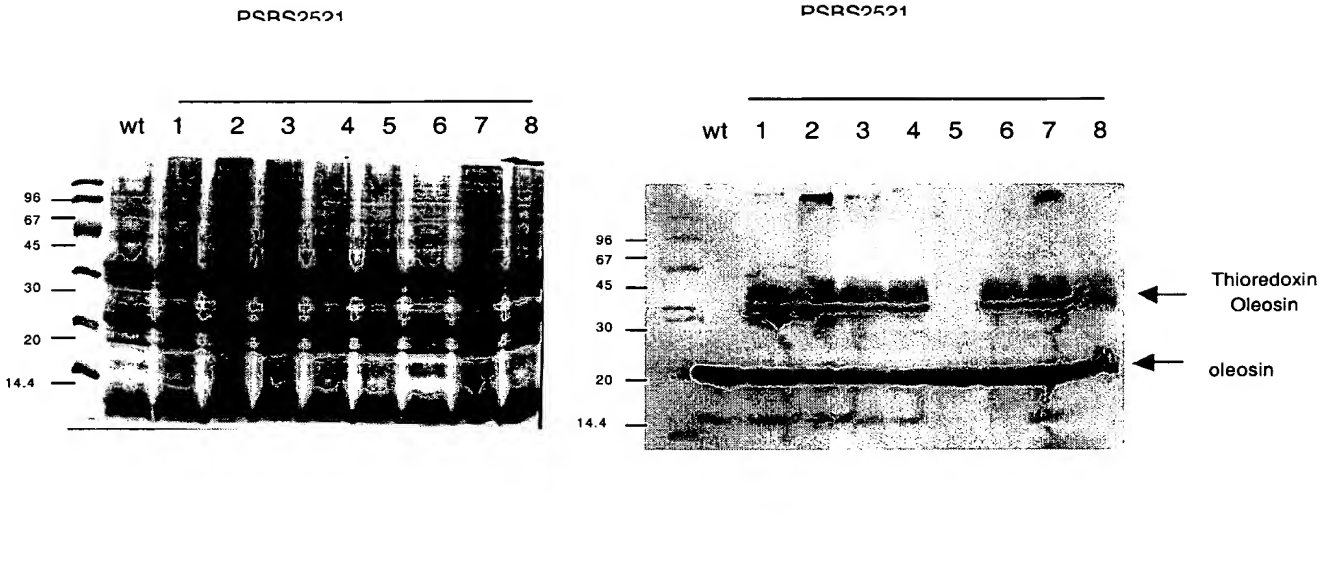

1 2 3
96
67
45
30
20
14.4
A
1 2 3
96
67
45
30
20
14.4
Oleosin thioredoxin
Oleosin
B

FIGURE 13


pSBS2521
wt 1 2 3 4 5 6 7 8
96
67
45
30
20
14.4
pSBS2521
wt 1 2 3 4 5 6 7 8
96
67
45
30
20
14.4
Thioredoxin
Oleosin
oleosin

A

B

FIGURE 14

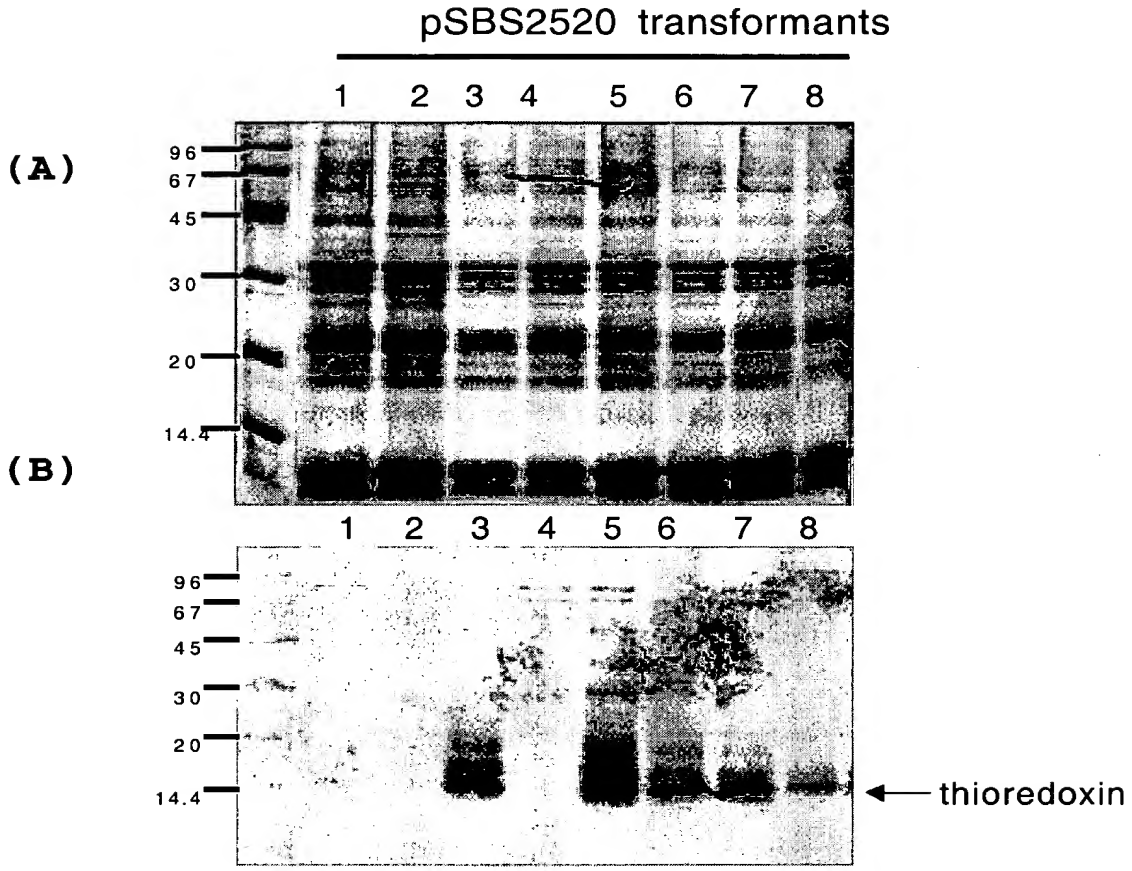

pSBS2520 transformants
1 2 3 4 5 6 7 8
(A)
96
67
45
30
20
14.4
(B)
1 2 3 4 5 6 7 8
96
67
45
30
20
14.4
thioredoxin

FIGURE 15

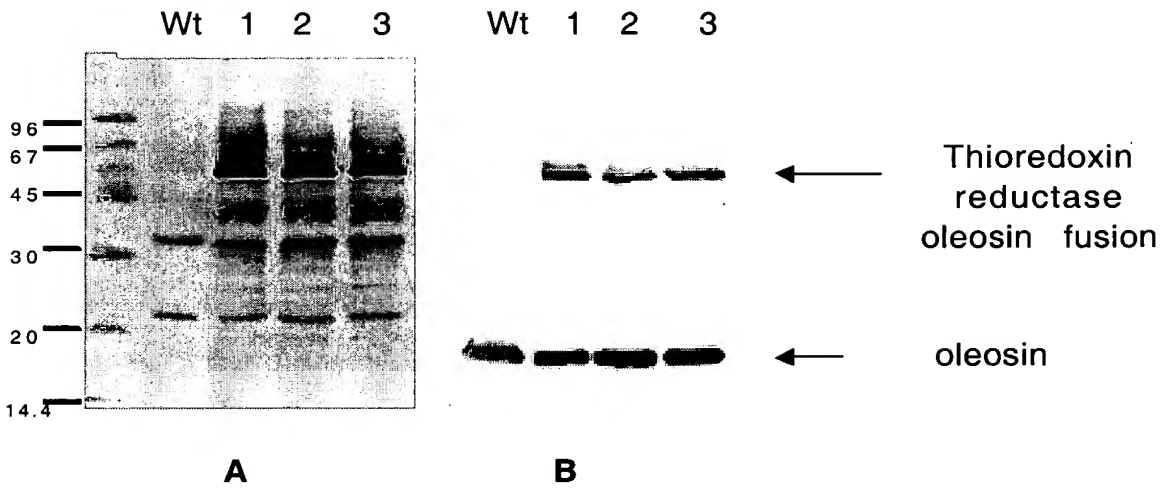
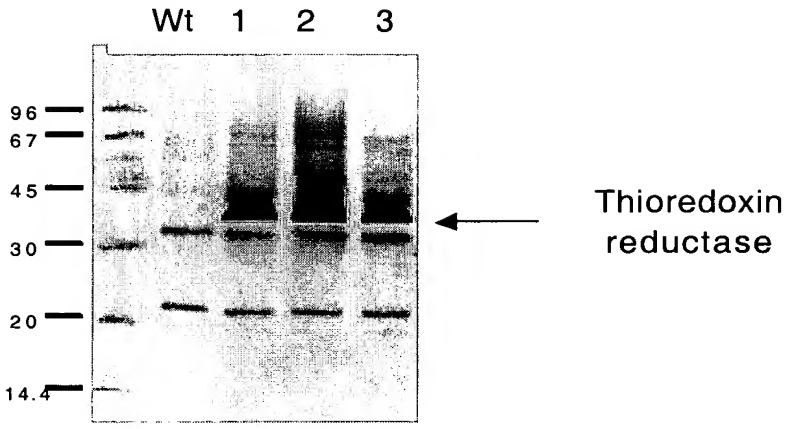
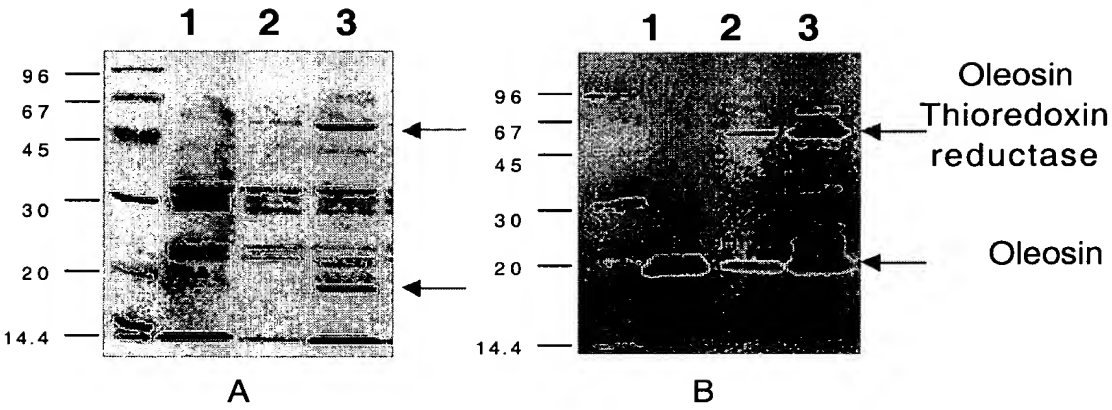

Wt 1 2 3
Wt 1 2 3
96
67
45
30
20
14.4
A
B
Thioredoxin reductase oleosin fusion
oleosin

FIGURE 16



1550200.060602

FIGURE 17


1 2 3
96
67
45
30
20
14.4
A
1 2 3
96
67
45
30
20
14.4
B
Oleosin
Thioredoxin
reductase
Oleosin